1600

RAW SEQUENCE LISTING   DATE: 04/17/2003
PATENT APPLICATION: US/09/679,687B   TIME: 12:02:56

Input Set : **A:\BB1162 US NA Corrected Seq Listing.txt**
Output Set: **N:\CRF4\04172003\I679687B.raw**

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      3 <110> APPLICANT: Allen, Stephen M.
      4        Hitz, William D.
      5        Rafalski, J. Antoni
      7 <120> TITLE OF INVENTION: SUCROSE TRANSPORT PROTEINS
      9 <130> FILE REFERENCE: BB1162 US NA
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/679,687B
C--> 12 <141> CURRENT FILING DATE: 2001-03-05
     14 <150> PRIOR APPLICATION NUMBER: 60/081,148
     15 <151> PRIOR FILING DATE: 1998-04-09
     17 <150> PRIOR APPLICATION NUMBER: PCT/US99/07562
     18 <151> PRIOR FILING DATE: 1999-04-07
     20 <160> NUMBER OF SEQ ID NOS: 28
     22 <170> SOFTWARE: Microsoft Office 97
     24 <210> SEQ ID NO: 1
     25 <211> LENGTH: 2088
     26 <212> TYPE: DNA
     27 <213> ORGANISM: Zea mays
     29 <400> SEQUENCE: 1
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     32 atcgatccta gctagctagc tagctagggc gcgaccgtcg tctcggtggt tgttgacagg  180
     33 tcccgtacgt gtgtgctcgc catggctcgt ggcgacggcg ggcagctggc ggagctgtcc  240
     34 gcgggggtcc gcggcgcggc cgcggtggtg gaccacgtgg ccccgatcag cctcgggagg  300
     35 ctcatcctcg ccggcatggt cgccggcggc gtgcagtacg gctgggcgct gcagctctcc  360
     36 ctcctcacgc cctacgtgca gactctgggg ctttcacatg cgctcacttc attcatgtgg  420
     37 ctctgcggcc ctattgccgg cttagtggtc caaccgctgg ttggcctgta cagcgacagg  480
     38 tgtacatcga gatggggag acggaggccg tttatcctga cagggtgcat gctcatctgc  540
     39 gttgccgtca ttgttgtcgg attctcgtca gacatcggag ctgctctagg ggacacgaag  600
     40 gaacactgca gcctctacca cggtcctcgt tggcacgctg cgatcgtgta cgttctgggg  660
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     42 gatctatgtg accatcatgg gccaagtgcg gctaactcca tcttctgttc ttggatggcg  780
     43 ctgggaaaca tcctaggcta ctcctctggc tccacgaaca attggcacaa gtggtttccc  840
     44 ttccttaaaa cgagcgcctg ctgtgaggcc tgtgcgaacc tgaaaggtgc atttctggtg  900
     45 gccgtggtgt tcctagtcct gtgcctgacg gtaaccctga tcttcgccaa ggaggtgccg  960
     46 tacagagcga acgagaacct cccgacgacg aaggccggcg cgaggtcga gactgagcct 1020
     47 accgggccac ttgccgtgct caagggcttc aaggacctgc ctcccgggat gccgtccgtg 1080
     48 ctcctcgtga ctgccatcac ctggctttcg tggttcccgt tcatcctcta cgacaccgac 1140
     49 tggatgggcc gggagatcta ccacggcgac cccaagggga gcaacgccca gatctcggcg 1200
     50 ttcaacgaag gtgtccgagt cggcgcgttc gggctgctac tcaactcggt tattctaggg 1260
     51 ttcagctcgt tcctgatcga gcccatgtgc cggaaggtcg ggccgaggggt ggtgtgggtg 1320
     52 acgagcaact tcatggtctg cgtcgccatg gcggccaccg cgctgatcag cttctggtcg 1380
     53 ctcaggact accacgggta cgtgcaggac gccatcaccg cgaacgccag catcaaggcc 1440
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ENTERED

P.6

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RAW SEQUENCE LISTING              DATE: 04/17/2003
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Output Set: N:\CRF4\04172003\I679687B.raw

55 ttcgcggtga cggcgcagct ggcggccacc cggggcggcg ggcaggggct gtgcaccggc 1560
56 gtcctcaaca tctccatcgt catccctcag gtgatcatcg cgctgggcgc cggcccgtgg 1620
57 gacgcgctgt tcgggaaggg caacatcccg gcgttcggcg tcgcgtcggc cttcgccctc 1680
58 gtcggcggcg tcgtgggcgt gttcctgctg cccaagatct ccaagcgcca gttccgggcc 1740
59 gtcagcgcgg gcggccactg atcgaacccg gccggggccg gccgccggca cgcagcccgg 1800
60 caagagctgt atgttgttga gagttgaaca gaaaccatgc atgtgtgctt ctgtagttct 1860
61 gttgtttgtg gtcgatcgat gggcgttgcg tggcagcgtg ggcaagcgag gcgaggtgcg 1920
62 cggatccaaa aaaagggcca ttcgatcaat caatgtgtag tagagtacaa ctagacgatg 1980
63 atgttcacat catttgtctt taatacatac cggtttctat tgtctttaaa aaaaaaaaa 2040
64 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa           2088
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67 <211> LENGTH: 519
68 <212> TYPE: PRT
69 <213> ORGANISM: Zea mays
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76              20                  25                  30
78 Arg Leu Ile Leu Ala Gly Met Val Ala Gly Gly Val Gln Tyr Gly Trp
79          35                  40                  45
81 Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln Thr Leu Gly Leu
82      50                  55                  60
84 Ser His Ala Leu Thr Ser Phe Met Trp Leu Cys Gly Pro Ile Ala Gly
85  65                  70                  75                  80
87 Leu Val Val Gln Pro Leu Val Gly Leu Tyr Ser Asp Arg Cys Thr Ser
88              85                  90                  95
90 Arg Trp Gly Arg Arg Arg Pro Phe Ile Leu Thr Gly Cys Met Leu Ile
91          100                 105                 110
93 Cys Val Ala Val Ile Val Val Gly Phe Ser Ser Asp Ile Gly Ala Ala
94          115                 120                 125
96 Leu Gly Asp Thr Lys Glu His Cys Ser Leu Tyr His Gly Pro Arg Trp
97      130                 135                 140
99 His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu Leu Asp Phe Ser
100 145                 150                 155                 160
102 Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Met Met Ala Asp Leu Cys
103              165                 170                 175
105 Asp His His Gly Pro Ser Ala Ala Asn Ser Ile Phe Cys Ser Trp Met
106              180                 185                 190
108 Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser Thr Asn Asn Trp
109          195                 200                 205
111 His Lys Trp Phe Pro Phe Leu Lys Thr Ser Ala Cys Cys Glu Ala Cys
112      210                 215                 220
114 Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Val Phe Leu Val Leu
115 225                 230                 235                 240
117 Cys Leu Thr Val Thr Leu Ile Phe Ala Lys Glu Val Pro Tyr Arg Ala
118              245                 250                 255
120 Asn Glu Asn Leu Pro Thr Thr Lys Ala Gly Gly Glu Val Glu Thr Glu
121              260                 265                 270
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123 Pro Thr Gly Pro Leu Ala Val Leu Lys Gly Phe Lys Asp Leu Pro Pro
124         275                 280                 285
126 Gly Met Pro Ser Val Leu Leu Val Thr Ala Ile Thr Trp Leu Ser Trp
127     290                 295                 300
129 Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg Glu Ile Tyr
130 305                 310                 315                 320
132 His Gly Asp Pro Lys Gly Ser Asn Ala Gln Ile Ser Ala Phe Asn Glu
133                 325                 330                 335
135 Gly Val Arg Val Gly Ala Phe Gly Leu Leu Leu Asn Ser Val Ile Leu
136             340                 345                 350
138 Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Arg Lys Val Gly Pro
139         355                 360                 365
141 Arg Val Val Trp Val Thr Ser Asn Phe Met Val Cys Val Ala Met Ala
142     370                 375                 380
144 Ala Thr Ala Leu Ile Ser Phe Trp Ser Leu Arg Asp Tyr His Gly Tyr
145 385                 390                 395                 400
147 Val Gln Asp Ala Ile Thr Ala Asn Ala Ser Ile Lys Ala Val Cys Leu
148                 405                 410                 415
150 Val Leu Phe Ala Phe Leu Gly Val Pro Leu Ala Ile Leu Tyr Ser Val
151             420                 425                 430
153 Pro Phe Ala Val Thr Ala Gln Leu Ala Ala Thr Arg Gly Gly Gly Gln
154         435                 440                 445
156 Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile Pro Gln Val
157     450                 455                 460
159 Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Ala Leu Phe Gly Lys Gly
160 465                 470                 475                 480
162 Asn Ile Pro Ala Phe Gly Val Ala Ser Ala Phe Ala Leu Val Gly Gly
163             485                 490                 495
165 Val Val Gly Val Phe Leu Leu Pro Lys Ile Ser Lys Arg Gln Phe Arg
166             500                 505                 510
168 Ala Val Ser Ala Gly Gly His
169         515
171 <210> SEQ ID NO: 3
172 <211> LENGTH: 825
173 <212> TYPE: DNA
174 <213> ORGANISM: Zea mays
176 <400> SEQUENCE: 3
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178 ggcaaataaa acagtcaaga tcacggcatt ggttgttttc tctcttctcg gattgccact  120
179 ctccatcact tacagcgttc cgttttctgt gactgctgag ctgactgccg gtacaggagg  180
180 tggacaaggt ttggccacag gagtcctaaa tcttgctatc gtggttcccc agatagtagt  240
181 gtcgcttgga gcaggtccat gggacgctct gtatggagga gggaataccc cggcgttcgt  300
182 cttggcttcg gtcttctccc tggcagcagg tgtgctcgca gttctcaagc tgccaaagct  360
183 gtccaactcg taccaatctg ccgggttcca tggatttggc tgatgctcat gcccaaaaca  420
184 cccccgtctg ccatgtaaaa catcacacca acacttggcc ccattttgcc attcgtttac  480
185 agagaaatga ttcttttttc ctcgtacaac tacagaataa tgacagtgaa agtaggagtt  540
186 taggtgagag agagagagag gctaggtagg ttgatgtgaa ggtgtaaaag ctgtatcctc  600
187 ctttttttgt ttttgttttt gtttttgaca gtgtatgtaa gagctgtcca caagaaaatt  660
188 tacaagtggt gtaacctgcc ctcgtttgta cattgtacta ctactacatg acaatcatat  720
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              Output Set: N:\CRF4\04172003\I679687B.raw
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190 atgaaaaaaa aaaaaaaaaa aaaaaaaact cgaaactagt tctct                  825
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193 <211> LENGTH: 133
194 <212> TYPE: PRT
195 <213> ORGANISM: Zea mays
197 <400> SEQUENCE: 4
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201 His Ile Ile Gly Ala Asn Lys Thr Val Lys Ile Thr Ala Leu Val Val
202                 20                  25                  30
204 Phe Ser Leu Leu Gly Leu Pro Leu Ser Ile Thr Tyr Ser Val Pro Phe
205             35                  40                  45
207 Ser Val Thr Ala Glu Leu Thr Ala Gly Thr Gly Gly Gly Gln Gly Leu
208         50                  55                  60
210 Ala Thr Gly Val Leu Asn Leu Ala Ile Val Val Pro Gln Ile Val Val
211  65                  70                  75                  80
213 Ser Leu Gly Ala Gly Pro Trp Asp Ala Leu Tyr Gly Gly Gly Asn Thr
214                 85                  90                  95
216 Pro Ala Phe Val Leu Ala Ser Val Phe Ser Leu Ala Ala Gly Val Leu
217             100                 105                 110
219 Ala Val Leu Lys Leu Pro Lys Leu Ser Asn Ser Tyr Gln Ser Ala Gly
220         115                 120                 125
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223      130
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226 <211> LENGTH: 1977
227 <212> TYPE: DNA
228 <213> ORGANISM: Zea mays
230 <400> SEQUENCE: 5
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233 ctggggctct cacatgccct cacttcattc atgtggctat gcggtcctat tgctggctta  180
234 gtggtccaac cgctggttgg cctgtacagc gataggtgca cagcaagatg gggaagacgc  240
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236 tcgtccgaca tcggagctgc tctaggggac acaaaggaac actgcagcct ctaccacggc  360
237 cctcgttggc atgctgcgat cgtgtacgtt ctggggtttt ggctccttga cttctccaac  420
238 aatactgtgc aaggtccagc gcgtgctatg atggctgatc tgtgcggtca tcatgggcct  480
239 agtgcagcca actcaatctt ctgttcttgg atggcgctgg gaaacatcct aggctattcc  540
240 tctggctcca caaacaactg gcacaagtgg tttccgttcc ttatgacaaa cgcgtgctgt  600
241 gaagcctgcg caaacctgaa aggcgcgttt ctggtggctg tggtgttcct aatcatgtgc  660
242 ttgactataa ccctgttctt cgccaaggaa gtgccctaca gaggaaacca gaacctcccc  720
243 acaaaggcaa acggcgaggt cgagactgaa ccttccggcc cactcgctgt gctcaagggc  780
244 ttcaagaact tgcccacggg gatgccgtcc gtgctcctcg taactggact cacctggctc  840
245 tcttggttcc cgttcatcct ctacgacacc gactggatgg ccgtgagat ctaccacggc  900
246 gaccccaagg gtagcaacgc tcagatctcg gcgttcgacg aaggcgtcag agttggctcg  960
247 ttcgggctgc tgctcaactc gatcgttcta ggattcagct cgttcctgat cgagcccatg 1020
248 tgccggaagg tcgggccgag ggtggtgtgg gtgacgagca acttcatggt ctgcgtcgcc 1080
249 atggcggcca ccgcgctgat cagcttctgg tcgctcaagg actaccacgg atacgtgcag 1140
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251 ggtgtccctc tcgccatcct gtacagcgtc ccgttcgcgg tgacggcgca gctggcggcc 1260
252 acgaagggcg gcgggcaggg gctgtgcacc ggcgtgctca acatctccat cgtcatccct 1320
253 caggtgatca tcgcgctggg cgcgggcccg tgggacgcgc tgttcggcaa gggcaacatc 1380
254 ccggcgttcg gcgtggcgtc ggggttcgcc ctcatcggcg gcgtcgtggg cgtgttcctg 1440
255 ctgcccaaga tctccaagcg ccagttccgc gccgtcagcg cgggcggcca ctgatcgcgg 1500
256 ccgccgcgcc ggagcacggc acggcggcac agcccagccg tgctagagct gtatgttttg 1560
257 aaagttgaaa cagaataaga agcgggcgaa acgagaaaac catgcatgtc atgtgtgtgc 1620
258 ttttgttgtg tgtggggtgg ggcaagcgag gcgaggtgtg tggaggtgaa gtgaaggtga 1680
259 gcatatccag caccagctgg taccaaggtc gggtctctgt gctagtgcta ttagctagtg 1740
260 taaggagcga gtaggtcagt taaggctggt gcgtcgtgag ggctgtcttg tgtgtagcta 1800
261 cagcagacgg ttcatcagaa ggattattcg tgcagtatat acagtacaac tagacaatga 1860
262 tgttgatgat tggtctagag ctagaggcct atagccctat actactgtgt attgtccgcc 1920
263 gttttagttt tttggtccca tcccatcaat gcaaccgcct tgttttaaaa aaaaaaa    1977
265 <210> SEQ ID NO: 6
266 <211> LENGTH: 497
267 <212> TYPE: PRT
268 <213> ORGANISM: Zea mays
270 <400> SEQUENCE: 6
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275             20                  25                  30
277 Leu Leu Thr Pro Tyr Val Gln Thr Leu Gly Leu Ser His Ala Leu Thr
278         35                  40                  45
280 Ser Phe Met Trp Leu Cys Gly Pro Ile Ala Gly Leu Val Val Gln Pro
281     50                  55                  60
283 Leu Val Gly Leu Tyr Ser Asp Arg Cys Thr Ala Arg Trp Gly Arg Arg
284 65                  70                  75                  80
286 Arg Pro Phe Ile Leu Ile Gly Cys Met Leu Ile Cys Leu Ala Val Ile
287                 85                  90                  95
289 Val Val Gly Phe Ser Ser Asp Ile Gly Ala Ala Leu Gly Asp Thr Lys
290             100                 105                 110
292 Glu His Cys Ser Leu Tyr His Gly Pro Arg Trp His Ala Ala Ile Val
293         115                 120                 125
295 Tyr Val Leu Gly Phe Trp Leu Leu Asp Phe Ser Asn Asn Thr Val Gln
296     130                 135                 140
298 Gly Pro Ala Arg Ala Met Met Ala Asp Leu Cys Gly His His Gly Pro
299 145                 150                 155                 160
301 Ser Ala Ala Asn Ser Ile Phe Cys Ser Trp Met Ala Leu Gly Asn Ile
302             165                 170                 175
304 Leu Gly Tyr Ser Ser Gly Ser Thr Asn Asn Trp His Lys Trp Phe Pro
305             180                 185                 190
307 Phe Leu Met Thr Asn Ala Cys Cys Glu Ala Cys Ala Asn Leu Lys Gly
308         195                 200                 205
310 Ala Phe Leu Val Ala Val Val Phe Leu Ile Met Cys Leu Thr Ile Thr
311     210                 215                 220
313 Leu Phe Phe Ala Lys Glu Val Pro Tyr Arg Gly Asn Gln Asn Leu Pro
314 225                 230                 235                 240
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 1007
Seq#:14; Xaa Pos. 311,321
Seq#:19; N Pos. 1093